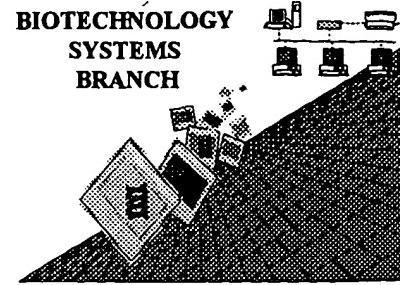


*Shah*

# RAW SEQUENCE LISTING

## ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/234,028A

Art Unit / Team No. :

162

Date Processed by STIC:

5/25/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

# Raw Sequence Listing Error Summary

---

**ERROR DETECTED**   **SUGGESTED**   **CORRECTION**SERIAL NUMBER: 09/234,028A**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8        Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10        Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)      (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/234,028ADATE: 05/25/1999  
TIME: 14:14:43

Input Set: I234028A.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

E--> 1 <110> > See item 13 on Error Summary Sheet  
 E--> 2 <120> for explanation of missing mandatory  
 W--> 3 <130> items, if file was created  
 4 <140> US/09/234,028A  
 5 <141> 1999-01-20  
 E--> 6 <160> Item 13 in Patent In 2.0

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES FOLLOW

E--> 7 <210> 2  
 8 <211> 456  
 9 <212> PRT  
 10 <213> Sus sp.  
 11 <400> 2

← See next page for explanation of errors

12 Met Asn Leu Asp Ile His Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr  
 13       1               5               10               15  
 14 Glu Leu Leu Pro Leu Leu Gln Gln Tyr Glu Val Val Arg Leu Asp Asp  
 15       20              25              30  
 16 Cys Gly Leu Thr Glu Glu His Cys Lys Asp Ile Gly Ser Ala Leu Arg  
 17       35              40              45  
 18 Ala Asn Pro Ser Leu Thr Glu Leu Cys Leu Arg Thr Asn Glu Leu Gly  
 19       50              55              60  
 20 Asp Ala Gly Val His Leu Val Leu Gln Gly Leu Gln Ser Pro Thr Cys  
 21       65              70              75              80  
 22 Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly  
 23       85              90              95  
 24 Cys Gly Val Leu Pro Ser Thr Leu Arg Ser Leu Pro Thr Leu Arg Glu  
 25       100             105             110  
 26 Leu His Leu Ser Asp Asn Pro Leu Gly Asp Ala Gly Leu Arg Leu Leu  
 27       115             120             125  
 28 Cys Glu Gly Leu Leu Asp Pro Gln Cys His Leu Glu Lys Leu Gln Leu  
 29       130             135             140  
 30 Glu Tyr Cys Arg Leu Thr Ala Ala Ser Cys Glu Pro Leu Ala Ser Val  
 31       145             150             155             160  
 32 Leu Arg Ala Thr Arg Ala Leu Lys Glu Leu Thr Val Ser Asn Asn Asp  
 33       165             170             175  
 34 Ile Gly Glu Ala Gly Ala Arg Val Leu Gly Gln Gly Leu Ala Asp Ser  
 35       180             185             190  
 36 Ala Cys Gln Leu Glu Thr Leu Arg Leu Glu Asn Cys Gly Leu Thr Pro  
 37       195             200             205  
 38 Ala Asn Cys Lys Asp Leu Cys Gly Ile Val Ala Ser Gln Ala Ser Leu  
 39       210             215             220

FYI ↴

Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

<210> 1 <Please insert delete - not used under new Sequence Rules

<211> ~~the mandatory~~ SEQUENCE LISTING

<212> PRT ~~the mandatory~~

<213> Rattus sp. ~~numerous identifiers and their responses~~

<400> 1

Met Ser Leu Asp Ile Gln Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr  
1 5 10 15

Glu Leu Leu Pro Leu Ile Gln Gln Tyr Gln Val Val Arg Leu Asp Asp  
20 25 30

Cys Gly Leu Thr Glu Val Arg Cys Lys Asp Ile Arg Ser Ala Ile Gln  
35 40 45

Ala Asn Pro Ala Leu Thr Glu Leu Ser Leu Arg Thr Asn Glu Leu Gly  
50 55 60

Asp Ala Gly Val Gly Leu Val Leu Gln Gly Leu Gln Asn Pro Thr Cys  
65 70 75 80

Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly  
85 90 95

Cys Gly Val Leu Pro Asp Val Leu Arg Ser Leu Ser Thr Leu Arg Glu  
100 105 110

Leu His Leu Asn Asp Asn Pro Leu Gly Asp Glu Gly Leu Lys Leu Leu  
115 120 125

Cys Glu Gly Leu Arg Asp Pro Gln Cys Arg Leu Glu Lys Leu Gln Leu  
130 135 140

Glu Tyr Cys Asn Leu Thr Ala Thr Ser Cys Glu Pro Leu Ala Ser Val  
145 150 155 160

Leu Arg Val Lys Pro Asp Phe Lys Glu Leu Val Leu Ser Asn Asn Asp  
165 170 175

Phe His Glu Ala Gly Ile His Thr Leu Cys Gln Gly Leu Lys Asp Ser  
180 185 190

Ala Cys Gln Leu Glu Ser Leu Lys Leu Glu Asn Cys Gly Ile Thr Ser  
195 200 205

Ala Asn Cys Lys Asp Leu Cys Asp Val Val Ala Ser Lys Ala Ser Leu  
210 215 220

Gln Glu Leu Asp Leu Gly Ser Asn Lys Leu Gly Asn Thr Gly Ile Ala  
225 230 235 240

Ala Leu Cys Ser Gly Leu Leu Pro Ser Cys Arg Leu Arg Thr Leu  
245 250 255

Trp Leu Trp Asp Cys Asp Val Thr Ala Glu Gly Cys Lys Asp Leu Cys  
260 265 270

Arg Val Leu Arg Ala Lys Gln Ser Leu Lys Glu Leu Ser Leu Ala Gly  
275 280 285

Asn Glu Leu Lys Asp Glu Gly Ala Gln Leu Leu Cys Glu Ser Leu Leu

290

295

300

Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val Lys Thr Cys Ser Leu  
305 310 315 320

Thr Ala Ala Ser Cys Pro His Phe Cys Ser Val Leu Thr Lys Asn Ser  
325 330 335

Ser Leu Phe Glu Leu Gln Met Ser Ser Asn Pro Leu Gly Asp Ser Gly  
340 345 350

Val Val Glu Leu Cys Lys Ala Leu Gly Tyr Pro Asp Thr Val Leu Arg  
355 360 365

Val Leu Trp Leu Gly Asp Cys Asp Val Thr Asp Ser Gly Cys Ser Ser  
370 375 380

Leu Ala Thr Val Leu Leu Ala Asn Arg Ser Leu Arg Glu Leu Asp Leu  
385 390 395 400

Ser Asn Asn Cys Met Gly Asp Asn Gly Val Leu Gln Leu Leu Glu Ser  
405 410 415

Leu Lys Gln Pro Ser Cys Ile Leu Gln Gln Leu Val Leu Tyr Asp Ile  
420 425 430

Tyr Trp Thr Asp Glu Val Glu Asp Gln Leu Arg Ala Leu Glu Glu Glu  
435 440 445

Arg Pro Ser Leu Arg Ile Ile Ser  
450 455